Please replace the paragraph beginning on page 12, line 10, with the following rewritten paragraph:

--Another preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., 1977, Nuc. Acids Res. 25:3389-3402 and Altschul et al., 1990, J. Mol. Biol. 215:403-410, respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the world wide website of the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always>0) and N (penalty score for mismatching residues; always<0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. U.S.A. 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.--

C2

Please replace the paragraph beginning on page 3, line 10, with the following rewritten paragraph:

-- In one aspect, the invention provides a CLASP-7 polynucleotide that encodes a polypeptide having the full-length sequence of SEQ ID NO:2. In another aspect, the invention provides a CLASP-7 polynucleotide having the full-length sequence of SEQ ID NO:1 or fragment thereof. In another aspect of the invention, the cDNA sequence (or protein coding sequence) is encoded by the inserts of AVC-PD23 (ATCC accession number PTA-2772) or AVC-PD24 (ATCC accession number PTA-2773).--

C3

Please replace the paragraph beginning on page 3, line 10, with the following rewritten paragraph:

-- In one aspect, the invention provides a CLASP-7 polynucleotide that encodes a polypeptide having the full-length sequence of SEQ ID NO:2. In another aspect, the invention provides a CLASP-7 polynucleotide having the full-length sequence of SEQ ID NO:1 or fragment thereof. In another aspect of the invention, the cDNA sequence (or protein coding sequence) is encoded by the inserts of AVC-PD23 (ATCC accession number PTA-2772) or AVC-PD24 (ATCC accession number PTA-2773).--

Please replace the paragraph beginning on page 111, line 18, with the following rewritten paragraph:

--CLASP proteins are described in commonly assigned Application Nos. 09/737,246, 09/736,969, 09/736,960, (all filed Dec. 13, 2000), 60/240,508, 60/240,503, 60/240,539, 60/240,543 (all filed Oct. 13, 2000); 09/547,276, 60/196,267, 60/196,527, 60/196,528, 60/196,460 (all filed Apr. 11, 2000); 60/182,296 (filed Feb. 14, 2000), 60/176,195 (filed Jan. 14, 2000), 60/170,453 (filed Dec. 13, 1999), 60/162,498 (filed Oct. 29, 1999), 60/160,860 filed Oct. 21, 1999, 60/129,171 filed Apr. 14, 1999, and in published PCT publications PCT/US00/13161 (WO 00/69896); PCT/US00/13205 (WO 00/69898); PCT/US00/13166 (WO 00/69897); PCT/US00/10158 (WO 00/61747); and PCT/US99/22996 (WO 00/20434). The disclosures of each of the aforementioned applications and publications is expressly incorporated herein by reference in its entirety for all purposes.--

Please replace the paragraph beginning on page 31, line 26, with the following rewritten paragraph:

--As is illustrated in FIG. 3, CLASP-7 is a member of a superfamily of immune-cell associated proteins with similar motifs (e.g., CLASP-1, 2/6, 3, 4, 5, 7). CLASP-1 is described in WO 00/20434. CLASP-1 uniquely among the known CLASPs contains SH3 binding domain motifs. CLASP-2 is described in WO 00/61747. CLASP-2 polypeptides have no adaptor binding sites or SH3 binding domains found in CLASP-1. Other CLASP family members are described in Application Nos. 09/737,246, 09/736,969, 09/736,960 (all filed Dec. 13, 2000), 60/240,508, 60/240,503, 60/240,503, 60/240,539, and 60/240,543 (all filed Oct. 13, 2000). The aforementioned publications and applications are all incorporated by reference herein in its entirely for all purposes.--